

Run on: November 29, 2001, 08:52:45 ; Search time 10554.9 Seconds
(without alignments)

10137.587 Million cell updates/sec

Title: US-09-526-329-40

Perfect score:	6486
Sequence:	1 ttctctctctccccctctc.....ggtcattcagcagcaggac 648

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing:	Minimum Match 0%
	Maximum Match 100%

Listing first 45 summaries

Database :

- 1: gb_ba:*
- 2: gb_hlg:*
- 3: gb_in:*
- 4: gb_cm:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_vl:*
- 14: gb_vl:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_com:*
- 20: em_or:*
- 21: em_ov:*
- 22: em_pat:*
- 23: em_ph:*
- 24: em_pl:*
- 25: em_ro:*
- 26: em_sts:*
- 27: em_sy:*
- 28: em_vl:*
- 29: em_vl:*
- 30: em_hlgo_hum:*
- 31: em_hlgo_in:*
- 32: em_hlgo_pl:*
- 33: em_hlg_hum:*
- 34: em_hlg_in:*
- 35: em_hlg_ro:*
- 36: em_hlg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
1	6485	100.0	6486	9	AF110465	AF110465 Homo sapi	
2	6443.8	99.3	166308	9	CNS01DX2	AL139020 Human chr	
3	6389.4	98.5	210791	9	CNS01DX2	AL133467 Human chr	
4	1633.4	25.2	1717	9	AB025272	AB025274 Homo sapi	
5	1338.4	20.6	1722	9	AB018635	AB018553 Homo sapi	
6	701.2	10.8	1152	9	AF110466	AF110466 Homo sapi	
7	701.2	10.8	3144	9	AB035343	AB035343 Homo sapi	
8	701.2	10.8	3240	9	AB035342	AB035342 Homo sapi	
9	701.2	10.8	3532	9	AB035340	AB035340 Homo sapi	
10	701.2	10.8	3599	9	AB035341	AB035341 Homo sapi	
11	699.8	10.8	1177	9	AF137027	AF137027 Homo sapi	
12	644.4	9.9	753	9	AB025272	AB025272 Homo sapi	
13	570.4	8.8	627	9	AC016603	AC016603 Homo sapi	
14	506	7.8	110879	9	AC010336	AC010336 Homo sapi	
15	506	7.8	114438	9	AC010339	AC010339 Homo sapi	
16	506	7.8	204843	9	AF110467	AF110467 Homo sapi	
17	497.6	7.7	1248	9	AC008889	AC008889 Homo sapi	
18	493.8	7.6	137808	9	AL360013	AL360013 Homo sapi	
19	478.6	7.6	155345	2	AL366788	AL356788 Homo sapi	
20	478.6	7.4	174095	2	AL366788	AL359184 Homo sapi	
21	474.8	7.3	172757	2	AL366788	AC0090127 Homo sapi	
22	472	7.2	192875	2	AC009117	AC011476 Homo sapi	
23	467.4	7.2	186497	2	AP003511	AP003531 Homo sapi	
24	467.4	7.2	154442	9	AC004859	AC004859 Homo sapi	
25	466.4	7.2	120766	9	AC004150	AC004150 Homo sapi	
26	466	7.1	224400	2	AC008758	AC008758 Homo sapi	
27	463	7.1	100732	2	AL133347	Human DNA	
28	462.6	7.1	100036	9	AP000557	AP000557 Homo sapi	
29	462.2	7.1	169997	9	AC008440	AC008440 Homo sapi	
30	462	7.1	169997	2	AC011501	AC011501 Homo sapi	
31	460.8	7.1	206836	2	AC021616	AC021616 Homo sapi	
32	459	7.1	171523	9	AC021616	AC021616 Homo sapi	
33	457.2	7.0	211544	9	AC021615	AC0090114 Homo sapi	
34	456	7.0	156311	2	AC0090114	AC0090114 Homo sapi	
35	454.8	7.0	169237	9	AC009516	AC009516 Homo sapi	
36	454.8	7.0	176051	9	AC023490	AC023490 Homo sapi	
37	454.6	7.0	212656	9	AC007957	AC007957 Homo sapi	
38	454.6	7.0	194618	9	AP000556	AP000556 Homo sapi	
39	454.4	7.0	157086	2	AP000552	AP000552 Homo sapi	
40	450.2	6.9	179250	9	AC0084291	AC0084291 Homo sapi	
41	448.6	6.9	212656	9	AC007957	AC007957 Homo sapi	
42	446.6	6.9	199287	9	AC023157	AC023157 Homo sapi	
43	444.6	6.9	157756	9	AC007003	AC007003 Homo sapi	
44	444	6.8	97078	9	AC005841	AC005841 Homo sapi	
45	443.6	6.8	172800	2	AL356597	Homo sapi	

ALIGNMENTS

RESULT	1
LOCUS	AF110465
DEFINITION	Homo sapiens T-cell leukemia/lymphoma 1B (TCL1B) gene, complete cds.
ACCESSION	AF110465
VERSION	AF110465.1
KEYWORDS	GI:4324702
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 6486) Pekarsky,Y., Hallas,C., Isobe,M., Russo,G. and Croce,C.M. Abnormalities at 14q32.1 in T cell malignancies involve two oncogenes Proc. Natl. Acad. Sci. U.S.A. 96 (6), 2949-2951 (1999)
JOURNAL	
MEDLINE	99170995
REFERENCE	2 (bases 1 to 6486)
AUTHORS	Pekarsky,Y., Hallas,C. and Croce,C.M.
AUTHORS	

Qy	661	gaagagaggttctccaggtcttagaagaagaggaagagtagtctaaagcaaaagatttgcag	720
Db	661	gagtagaagatttctccaggtcttagaagaagaggaagagtagtctaaagcaaaagatttgcag	720
Qy	721	ccctgagagaccaggtgggccaacaaggatgaacatgatcatgtgtctcagatctcgtatct	780
Db	721	ccctgagagaccaggtgggccaacaaggatgaacatgatcatgtgtctcagatctcgtatct	780
Qy	781	gcaaaatgagaataataaccctcgtgtgcaagatgtaacacagatctccatatacag	840
Db	781	gcaaaatgagaataataataaccctcgtgtgcaagatgtaacacagatctccatatacag	840
Qy	841	ctcaccgctgtaatgacctcgggggaaagcatttgcgtacaacagatcttcggaatatattc	900
Db	841	ctcaccgctgtaatgacctcgggggaaagcatttgcgtacaacagatcttcggaatatattc	900
Qy	901	aggagctcgggtgtagtccctagatcttcttacttcttcaaaagctccccaagttgatacga	960
Db	901	aggagctcgggtgtagtccctagatcttcttacttcttcaaaagctccccaagttgatacga	960
Qy	961	taagagctaaagaaacggcgtctagaatgagggcctttagatccacagcagctcttaagagat	1020
Db	961	taagagctaaagaaacggcgtctagaatgagggcctttagatccacagcagctcttaagagat	1020
Qy	1021	gaagtaatacagtagcgtctctctgtgtgtggtgcgtgggaaatgattccagagccga	1080
Db	1021	gaagtaatacagtagcgtctctctgtgtgtggtgcgtgggaaatgattccagagccga	1080
Qy	1081	ctgctgagctcctaactcccgatagaagaatactctggtgtagtaatactacataaccctcag	1140
Db	1081	ctgctgagctcctaactcccgatagaagaatactctggtgtagtaatactacataaccctcag	1140
Qy	1141	cgcatctctactaatatttbaaataagaattactaaataaacctatagctacacacttaaca	1200
Db	1141	cgcatctctactaatatttbaaataagaattactaaataaacctatagctacacacttaaca	1200
Qy	1201	tcacttcaagctctcgtcttcttggaaacttttggaaattcttcttttcccaataattctt	1260
Db	1201	tcacttcaagctctcgtcttcttggaaacttttggaaattcttcttttcccaataattctt	1260
Qy	1261	aatctcggagttctagtcgaattcatgggtgcgaatcatcatgaaatggggggcgtgcgtctac	1320
Db	1261	aatctcggagttctagtcgaattcatgggtgcgaatcatcatgaaatggggggcgtgcgtctac	1320
Qy	1321	cttgatgaatgttgaagaagcgttcccgagatatttaaaatggcatttggctctggcgcgc	1380
Db	1321	cttgatgaatgttgaagaagcgttcccgagatatttaaaatggcatttggctctggcgcgc	1380
Qy	1381	ggtgagctcaagcgtctaatcccgacattctgggaagccgagatggcgttatacagaatc	1440
Db	1381	ggtgagctcaagcgtctaatcccgacattctgggaagccgagatggcgttatacagaatc	1440
Qy	1441	aggaaacacgagaccatccatgccaacaatggggaaacccgctctactataaataatcaaaa	1500
Db	1441	aggaaacacgagaccatccatgccaacaatggggaaacccgctctactataaataatcaaaa	1500
Qy	1501	aattgaccgggctgtgtgtggcgagcgtctgtatgtccagctatctcgggaagctggaagcag	1560
Db	1501	aattgaccgggctgtgtgtggcgagcgtctgtatgtccagctatctcgggaagctggaagcag	1560
Qy	1561	agaaatgagcagaaacccggagaggaagccttctagtagacggagatgcacacatgcac	1620
Db	1561	agaaatgagcagaaacccggagaggaagccttctagtagacggagatgcacacatgcac	1620
Qy	1621	cagctctgggtgaagaagtggaagatcgtgtcccaaaaaaataaaaaaataatggcgttt	1680
Db	1621	cagctctgggtgaagaagtggaagatcgtgtcccaaaaaaataaaaaaataatggcgttt	1680
Qy	1681	aggtctcttgataaacaattaccatgcgtgttctgttcttcttgagaagaagctctgcctgt	1740
Db	1681	aggtctcttgataaacaattaccatgcgtgttctgttcttcttgagaagaagctctgcctgt	1740

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Db	2821	CTACTAAATAATCAAAAATAATTGCGCGGTGCGGTGCGGGGCTGTGTAGTCCCAATCAC	2880
Qy	2881	tcggggagctcgagagcagaaatgacttgaacccggagagcgagacttgcagtgagctcga	2940
Db	2881	TCGGGGGGCTGAGGACGAGAGATGCTTGAACCTGGAGGCGGAGACTTCGACGTAGACTCGA	2940
Qy	2941	gattccagccacctgcgaccccgactggggagacagagcagaacccggtccaaacaacaa	3000
Db	2941	GATCCAGCCACTGCACCTCGACCTGGAGCAGACAGACAGCTCCCTCTCAACAAACAA	3000
Qy	3001	agcaaaaacaaaaaacagttaaagattttttttttttaaagtctcagtggaatagaa	3060
Db	3001	AGCAAAAACAAAAAACAGTTAAGATTTTTTTTTTTTTTAAATGATCTAGTGAATAATGA	3060
Qy	3061	atggatctctcaaaataacttagccaggggtcgaga taaggagacctctgaatgaatttt	3120
Db	3061	ATGGATCTCTCAAAATAACTTAGCCAGCGGGGTGAATAGGAGACCTACTAGTAATGATTTT	3120
Qy	3121	ttccctctttctttaaataatgatgatgtcttaaggtgggaatttgcttccgtggcg	3180
Db	3121	TTCCCTCTCTTCTTAAATAATGATGTAGTCTTGAAGGAGTAATGAGCTCTTGAGGCG	3180
Qy	3181	acacatactaatgcaaaagatcagccactttctctgaagaagatctgaatggtaaacattt	3240
Db	3181	ACACATCTAATGCAAAAGATCAGCCACTTTTCTGTAAAGATCTGATGCTAAACATTTT	3240
Qy	3241	ccacttgaagatcgtcctcttgcagtaactcagctcgtcacttgcattgcagtgaaaagacgt	3300
Db	3241	CCACTTGAAGATATGCTCTTGCAGGCTACTCAGCTCTGCTATTGCAATGCAAGTAAGCAGCT	3300
Qy	3301	aaagcgcaacggtcaaaagaaatgaacggagagagccttagttatttcaataaagcttatt	3360
Db	3301	AAAGCGCAACGGTCAAAAGAAATGACGGAAGAGCGCTTAATTTATTTTCAATTAACCTTTAT	3360
Qy	3361	tgcaaaagacaga tgcagacagacactagtttgcgcactctgtactacagtlccagaataca	3420
Db	3361	TGCAAAAACGATGCAACGCAACGACTTAGTTGCTGATCTCTGATCTAAGTCAGATATACA	3420
Qy	3421	caggaagagagagcttctgcgcgtataacttaactctctcttgcgaagaagagcact	3480
Db	3421	CAGGAGAGGAGAGATTTGGCCGATATATTTAATTAATCTTCTCTTGGCAAAAGCAGTCCAT	3480
Qy	3481	aaaaaaaaggaggaacaacaactcgagaaaaattctcaacaatgctcgtatgatagagc	3540
Db	3481	AAAAAAAAGTAGAGCAACAACATCGAATAAAATTTATTCACAACATCTGATGATGATGAGAC	3540
Qy	3541	actaatcttcttaattcaataaagaacttttcaacaagaagaacaatacttagaaat	3600
Db	3541	ACTAATTTCTTAATTTCAAAAAGACATTTTATCTCAAAAAGAAACAAATCTAGAAAT	3600
Qy	3601	tgtcgaagaagacttccacttgttgcataacgttagaagagcttggattactttccca	3660
Db	3601	TGTGCAAAAGACTTCCATTTGTGTGCATAACGTAGAGAACTTGGTTTACTTTCCCA	3660
Qy	3661	tcaactcttcaactccagtaaccaagcctcaatttgtattttlatlatlatatgtaattatt	3720
Db	3661	TCACTCTTCTAATCTTCCAGTACAGCTCAATATTTGTATTTTATTTATTTATTTATTTATTT	3720
Qy	3721	ttcgagacaagcttgcgcgtgtctccagactcgtagtgcagtcagtcgtcgaatagctaac	3780
Db	3721	TTTGAGACAGAGCTTGTGCTGTCTTCCAGAGCTGAGTGCAGTGAACCTGACGATAGCTTAC	3780
Qy	3781	aacagagcttcaactccaggtgtcaagaatacttcaactgtgacttccgagtagctgg	3840
Db	3781	AACAGCTCTACTCCAGGTCAAAAATCTTCACTTACCTTACCTTCCCGATAGCTGAG	3840
Qy	3841	acgttaagacaatgcacacatgacagtaactttttattttcttgtagaagaagctc	3900
Db	3841	ACTGTAGGACACTGACCAACTGCGCAGCAATTTTATTTTGTGAGAACGATCTTC	3900
Qy	3901	attatgttcgcaagcgctgactgactcgttgcttgaagcagctcccgctgctgct	3960

